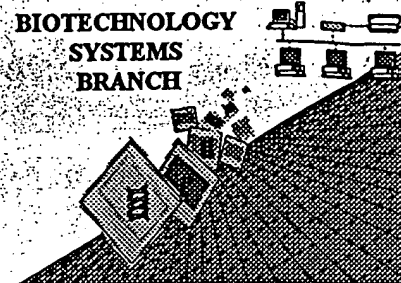


re-run Mikodem

RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/388,221
Art Unit / Team No. : /600
Date Processed by STIC: 9/15/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/388,221

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☒ **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) 10, 12. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ **Skipped Sequences (OLD RULES)** Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xI) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ **Skipped Sequences (NEW RULES)** Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ **Use of <213>Organism (NEW RULES)** Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ **Use of <220>Feature (NEW RULES)** Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ **PatentIn ver. 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/388,221

DATE: 09/15/1999
TIME: 12:43:26

Input Set: I388221.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

see p 6, 8-9

1 <110> Reed, John C.
2 <120> Novel Card Proteins Involved in Cell Death Regulation
3 <130> P-LJ 3650
4 <140> US/09/388,221
5 <141> 1999-09-01
6 <160> 18
7 <170> PatentIn Ver. 2.0

ERRORED SEQUENCES FOLLOW

8 <210> 11
9 <211> 4466
10 <212> DNA
11 <213> Artificial Sequence
12 <220>
13 <221> CDS
14 <222> (1)..(4275)
15 <220>
16 <223> Description of Artificial Sequence: Synthetic
17 Construct
18 <400> 11
19 atg gct ggc gga gcc tgg ggc cgc ctg gcc tgt tac ttg gag ttc ctg 48
20 Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu
21 1 5 10 15
22 aag aag gag gag ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg 96
23 Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala
24 20 25 30
25 cac tcc agg agc tct tcg ggt gag aca ccc gct cag cca gag aag acg 144
26 His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
27 35 40 45
28 agt ggc atg gag gtg gcc tcg tac ctg gtg gct cag tat ggg gag cag 192
29 Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
30 50 55 60
31 cgg gcc tgg gac cta gcc ctc cat acc tgg gag cag atg ggg ctg agg 240
32 Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg
33 65 70 75 80
34 tca ctg tgc gcc caa gcc cag gaa ggg gca ggc cac tct ccc tca ttc 288
35 Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe
36 85 90 95
37 ccc tac agc cca agt gaa ccc cac ctg ggg tct ccc agc caa ccc acc 336
38 Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr
39 100 105 110

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 RAW SEQUENCE LISTING
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40	tcc acc gca gtg cta atg ccc tgg atc cat gaa ttg ccg gcg ggg tgc	384
41	Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys	
42	115 120 125	
43	acc cag ggc tca gag aga agg gtt ttg aga cag ctg cct gac aca tct	432
44	Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser	
45	130 135 140	
46	gga cgc cgc tgg aga gaa atc tct gcc tca ctc ctc tac caa gct ctt	480
47	Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu	
48	145 150 155 160	
49	cca agc tcc cca gac cat gag tct cca agc cag gag tca ccc aac gcc	528
50	Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala	
51	165 170 175	
52	ccc aca tcc aca gca gtg ctg ggg agc tgg gga tcc cca cct cag ccc	576
53	Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro	
54	180 185 190	
55	agc cta gca ccc aga gag cag gag gct cct ggg acc caa tgg cct ctg	624
56	Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu	
57	195 200 205	
58	gat gaa acg tca gga att tac tac aca gaa atc aga gaa aga gag aga	672
59	Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg	
60	210 215 220	
61	gag aaa tca gag aaa ggc agg ccc cca tgg gca gcg gtg gta gga acg	720
62	Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr	
63	225 230 235 240	
64	ccc cca cag gcg cac acc agc cta cag ccc cac cac cac cca tgg gag	768
65	Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu	
66	245 250 255	
67	cct tct gtg aga gag agc ctc tgt tcc aca tgg ccc tgg aaa aat gag	816
68	Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu	
69	260 265 270	
70	gat ttt aac caa aaa ttc aca cag ctg cta ctt cta caa aga cct cac	864
71	Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His	
72	275 280 285	
73	ccc aga agc caa gat ccc ctg gtc aag aga agc tgg cct gat tat gtg	912
74	Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val	
75	290 295 300	
76	gag gag aat cga gga cat tta att gag atc aga gac tta ttt ggc cca	960
77	Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro	
78	305 310 315 320	
79	ggc ctg gat acc caa gaa cct cgc ata gtc ata ctg cag ggg gct gct	1008
80	Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala	
81	325 330 335	
82	gga att ggg aag tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg	1056
83	Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly	
84	340 345 350	
85	aga ggc cag ctg tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc	1104
86	Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser	
87	355 360 365	
88	tgc aga gag ctg gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc	1152
89	Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile	

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90	370	375	380	
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93	385 390 395 400			
94	agg cca gag cgg ctg ctc ttc atc ctc gat ggt gta gat gag cca gga	1248		
95	Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly			
96	405 410 415			
97	tgg gtc ttg cag gag ccg agt tct gag ctc tgt ctg cac tgg agc cag	1296		
98	Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln			
99	420 425 430			
100	cca cag ccg gcg gat gca ctg ctg ggc agt ttg ctg ggg aaa act ata	1344		
101	Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile			
102	435 440 445			
103	ctt ccc gag gca tcc ttc ctg atc acg gct cgg acc aca gct ctg cag	1392		
104	Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln			
105	450 455 460			
106	aac ctc att cct tct ttg gag cag gca cgt tgg gta gag gtc ctg ggg	1440		
107	Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly			
108	465 470 475 480			
109	ttc tct gag tcc agc agg aag gaa tat ttc tac aga tat ttc aca gat	1488		
110	Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp			
111	485 490 495			
112	gaa agg caa gca att aga gcc ttt agg ttg gtc aaa tca aac aaa gag	1536		
113	Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu			
114	500 505 510			
115	ctc tgg gcc ctg tgt ctt gtg ccc tgg gtg tcc tgg ctg gcc tgc act	1584		
116	Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr			
117	515 520 525			
118	tgc ctg atg cag cag atg aag ccg aag gaa aaa ctc aca ctg act tcc	1632		
119	Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser			
120	530 535 540			
121	aag acc acc aca acc ctc tgt cta cat tac ctt gcc cag gct ctc caa	1680		
122	Lys Thr Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln			
123	545 550 555 560			
124	gct cag cca ttg gga ccc cag ctc aga gac ctc tgc tct ctg gct gct	1728		
125	Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala			
126	565 570 575			
127	gag ggc atc tgg caa aaa aag acc ctt ttc agt cca gat gac ctc agg	1776		
128	Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg			
129	580 585 590			
130	aag cat ggg tta gat ggg gcc atc atc tcc acc ttc ttg aag atg ggt	1824		
131	Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly			
132	595 600 605			
133	att ctt caa gag cac ccc atc cct ctg agc tac agc ttc att cac ctc	1872		
134	Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu			
135	610 615 620			
136	tgt ttc caa gag ttc ttt gca gca atg tcc tat gtc ttg gag gat gag	1920		
137	Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu			
138	625 630 635 640			
139	aag ggg aga ggt aaa cat tct aat tgc atc ata gat ttg gaa aag acg	1968		

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140	Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr	
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142	cta gaa gca tat gga ata cat ggc ctg ttt ggg gca tca acc aca cgt	2016
143	Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg	
144	660 665 670	
145	ttc cta ttg ggc ctg tta agt gat gag ggg gag aga gag atg gag aac	2064
146	Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn	
147	675 680 685	
148	atc ttt cac tgc cgg ctg tct cag ggg agg aac ctg atg cag tgg gtc	2112
149	Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val	
150	690 695 700	
151	ccg tcc ctg cag ctg ctg ctg cag cca cac tct ctg gag tcc ctc cac	2160
152	Pro Ser Leu Gln Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His	
153	705 710 715 720	
154	tgc ttg tac gag act cgg aac aaa acg ttc ctg aca caa gtg atg gcc	2208
155	Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala	
156	725 730 735	
157	cat ttc gaa gaa atg ggc atg tgt gta gaa aca gac atg gag ctc tta	2256
158	His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu	
159	740 745 750	
160	gtg tgc act ttc tgc att aaa ttc agc cgc cac gtg aag aag ctt cag	2304
161	Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln	
162	755 760 765	
163	ctg att gag ggc agg cag cac aga tca aca tgg agc ccc acc atg gta	2352
164	Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val	
165	770 775 780	
166	gtc ctg ttc agg tgg gtc cca gtc aca gat gcc tat tgg cag att ctc	2400
167	Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu	
168	785 790 795 800	
169	ttc tcc gtc ctc aag gtc acc aga aac ctg aag gag ctg gac cta agt	2448
170	Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser	
171	805 810 815	
172	gga aac tcg ctg agc cac tct gca gtg aag agt ctt tgt aag acc ctg	2496
173	Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu	
174	820 825 830	
175	aga cgc cct cgc tgc ctc ctg gag acc ctg cgg ttg gct ggc tgt ggc	2544
176	Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly	
177	835 840 845	
178	ctc aca gct gag gac tgc aag gac ctt gcc ttt ggg ctg aga gcc aac	2592
179	Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn	
180	850 855 860	
181	cag acc ctg acc gag ctg gac ctg agc ttc aat gtg ctc acg gat gct	2640
182	Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala	
183	865 870 875 880	
184	gga gcc aaa cac ctt tgc cag aga ctg aga cag ccg agc tgc aag cta	2688
185	Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu	
186	885 890 895	
187	cag cga ctg cag ctg gtc agc tgt ggc ctc acg tct gac tgc tgc cag	2736
188	Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln	
189	900 905 910	

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191	Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp	
192	915 920 925	
193	ctg cag cag aac aac ctg gat gac gtt ggc gtg cga ctg ctc tgt gag	2832
194	Leu Gln Gln Asn Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu	
195	930 935 940	
196	ggg ctc agg cat cct gcc tgc aaa ctc ata cgc ctg ggg aaa cca agt	2880
197	Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Lys Pro Ser	
198	945 950 955 960	
199	gtg atg acc cct act gag ggc ctg gat acg gga gag atg agt aat agc	2928
200	Val Met Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser	
201	965 970 975	
202	aca tcc tca ctc aag cgg cag aga ctc gga tca gag agg gcg gct tcc	2976
203	Thr Ser Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser	
204	980 985 990	
205	cat gtt gct cag gct aat ctc aaa ctc ctg gac gtg agc aag atc ttc	3024
206	His Val Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe	
207	995 1000 1005	
208	cca att gct gag att gca gag gaa agc tcc cca gag gta gta ccg gtg	3072
209	Pro Ile Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val	
210	1010 1015 1020	
211	gaa ctc ttg tgc gtg cct tct cct gcc tct caa ggg gac ctg cat acg	3120
212	Glu Leu Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr	
213	1025 1030 1035 1040	
214	aag cct ttg ggg act gac gat gac ttt ctg ggg cct gaa gga aat gtg	3168
215	Lys Pro Leu Gly Thr Asp Asp Asp Phe Leu Gly Pro Glu Gly Asn Val	
216	1045 1050 1055	
217	gat gtt gag ttg att gat aag agc aca aac aga tac agc gtt tgg ttc	3216
218	Asp Val Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser Val Trp Phe	
219	1060 1065 1070	
220	ccc act gct ggc tgg tat ctg tgg tca gcc aca ggc ctc ggc ttc ctg	3264
221	Pro Thr Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu Gly Phe Leu	
222	1075 1080 1085	
223	gta agg gat gag gtc aca gtg acg att gcg ttt ggt tcc tgg agt cag	3312
224	Val Arg Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser Trp Ser Gln	
225	1090 1095 1100	
226	cac ctg gcc ctg gac ctg cag cac cat gaa cag tgg ctg gtg ggc ggc	3360
227	His Leu Ala Leu Asp Leu Gln His His Glu Gln Trp Leu Val Gly Gly	
228	1105 1110 1115 1120	
229	ccc ttg ttt gat gtc act gca gag cca gag gag gct gtc gcc gaa atc	3408
230	Pro Leu Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val Ala Glu Ile	
231	1125 1130 1135	
232	cac ctc ccc cac ttc atc tcc ctc caa ggt gag gtg gac gtc tcc tgg	3456
233	His Leu Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp Val Ser Trp	
234	1140 1145 1150	
235	ttt ctc gtt gcc cat ttt aag aat gaa ggg atg gtc ctg gag cat cca	3504
236	Phe Leu Val Ala His Phe Lys Asn Glu Gly Met Val Leu Glu His Pro	
237	1155 1160 1165	
238	gcc cgg gtg gag cct ttc tat gct gtc ctg gaa agc ccc agc ttc tct	3552
239	Ala Arg Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro Ser Phe Ser	

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RAW SEQUENCE LISTING
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243	1185	1190	1195	1200
244	ccc atc act tcc aac aca ttg atc tat tat cac ccc cac ccc gaa gat			3648
245	Pro Ile Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His Pro Glu Asp			
246		1205	1210	1215
247	att aag ttc cac ttg tac ctt gtc ccc agc gac gcc ttg cta aca aag			3696
248	Ile Lys Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu Leu Thr Lys			
249		1220	1225	1230
250	gcg ata gat gat gag gaa gat cgc ttc cat ggt gtg cgc ctg cag act			3744
251	Ala Ile Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg Leu Gln Thr			
252		1235	1240	1245
253	tcg ccc cca atg gaa ccc ctg aac ttt ggt tcc agt tat att gtg tct			3792
254	Ser Pro Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr Ile Val Ser			
255		1250	1255	1260
256	aat tct gct aac ctg aaa gta atg ccc aag gag ttg aaa ttg tcc tac			3840
257	Asn Ser Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys Leu Ser Tyr			
258		1265	1270	1275
259	agg agc cct gga gaa att cag cac ttc tca aaa ttc tat gct ggg cag			3888
260	Arg Ser Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr Ala Gly Gln			
261		1285	1290	1295
262	atg aag gaa ccc att caa ctt gag att act gaa aaa aga cat ggg act			3936
263	Met Lys Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg His Gly Thr			
264		1300	1305	1310
265	ttg gtg tgg gat act gag gtg aag cca gtg gat ctc cag ctt gta gct			3984
266	Leu Val Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln Leu Val Ala			
267		1315	1320	1325
268	gca tca gcc cct cct cct ttc tca ggt gca gcc ttt gtg aag gag aac			4032
269	Ala Ser Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val Lys Glu Asn			
270		1330	1335	1340
271	cac cgg caa ctc caa gcc agg atg ggg gac ctg aaa ggg gtg ctc gat			4080
272	His Arg Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp			
273		1345	1350	1355
274	gat ctc cag gac aat gag gtt ctt act gag aat gag aag gag ctg gtg			4128
275	Asp Leu Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val			
276		1365	1370	1375
277	gag cag gaa aag aca cgg cag agc aag aat gag gcc ttg ctg agc atg			4176
278	Glu Gln Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu Leu Ser Met			
279		1380	1385	1390
280	gtg gag aag aaa ggg gac ctg gcc ctg gac gtg ctc ttc aga agc att			4224
281	Val Glu Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe Arg Ser Ile			
282		1395	1400	1405
283	agt gaa agg gac cct tac ctc gtg tcc tat ctt aga cag cag aat ttg			4272
284	Ser Glu Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln Gln Asn Leu			
285		1410	1415	1420
286	taa aatgagtcag ttaggtagtc tggaagagag aatccagcgt tctcattgga			4325
287	<u>1425</u> delete - do not insert number if no amino acid is present			
288	aatggataaa cagaaatgtg atcattgatt tcagtgttca agacagaaga agactgggta			4385
289	acatctatca cacaggcttt caggacagac ttgtaacctg gcatgtacct attgactgta			4445

E-->

Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

LFYI

OIPE

PAGE: 7

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/388,221

DATE: 09/15/1999
TIME: 12:43:26

Input Set: I388221.RAW

290

tcctcatgca ttttcctcaa g

4466

09/388,721

8

<210> 10

<211> 1454

<212> PRT

<213> Artificial Sequence

all item 7 on Ena summary sheet

<400> 10

Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu
1 5 10 15

09/38221

9

<210> 12
<211> 1424
<212> PRT

<213> Artificial Sequence

all seen?

<400> 12

Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu
1 5 10 15